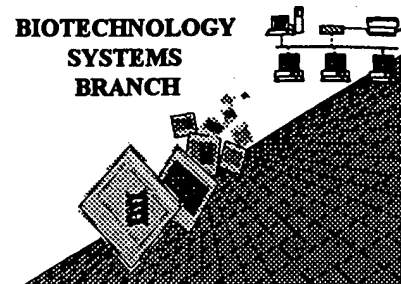


Hayes

# **RAW SEQUENCE LISTING** **ERROR REPORT**



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 08/803,954  
Art Unit / Team No. : 1645  
Date Processed by STIC: 3/31/99

**THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.**

**PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,**
- 2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY**

**THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.**

**IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:**

**ARTI SHAH 703-308-4212**

# Raw Sequence Listing Error Summary

## ERROR DETECTED   SUGGESTED   CORRECTION

SERIAL NUMBER: 08/803954

**ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE**

- 1        **Wrapped Nucleics**      The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
  
- 2        **Wrapped Aminos**      The amino acid number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
  
- 3        **Incorrect Line Length**      The rules require that a line not exceed 72 characters in length. This includes spaces.  
All text must be visible on page.
  
- 4        **Misaligned Amino Acid Numbering**      The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and uses spacing between the numbers.
  
- 5        **Non-ASCII**      This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
  
- 6        **Variable Length**      Sequence(s)        contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and indicate in the (ix) features section that some may be missing.
  
- 7        **Wrong Designation**      Sequence(s)        contain amino acid or nucleic acid designators which are not standard representations as per the Sequence Rules (Please refer to paragraph 1.822)
  
- 8        **Skipped Sequences (OLD RULES)**      Sequence(s)        missing. If intentional, please use the following format for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X:  
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
(x1) SEQUENCE DESCRIPTION:SEQ ID NO:X:  
This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
  
- 9        **Skipped Sequences (NEW RULES)**      Sequence(s)        missing. If intentional, please use the following format for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
  
- 10        **Use of n's or Xaa's (NEW RULES)**      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
  
- 11        **Use of <213>Organism (NEW RULES)**      Sequence(s)        are missing this mandatory field or its response.
  
- 12        **Use of <220>Feature (NEW RULES)**      Sequence(s)        are missing the <220>Feature and associated headings.  
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)  
(Sec. 1.823 of new Sequence Rules)
  
- 13        **PatentIn ver. 2.0 "bug"**      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).  
Instead, please use "File Manager" or any other means to copy file to floppy disk.